

2070 2079 2088 2097 2106 2115 2124 2133 R cGc cGc GGA GAT GTT ACC CTG CAC GCC GAT GCT ATC CAC AGA GGT GGA GGA CAA GTC ATT CCA ACC ATG AAG AGA D L Н Α D Α I H R G G G Q V I рт м к 690 700

SEQ ID NO:10

FIG. 1

mRNA	-54	mRNA -54 ACTITGAAGTICTIAATTITIGITCCTCGTAGAAGAACGCATAGATAATT -5	- 5
gDNA			
	7		q.
		 CAAA ATGG<u>GTATGT</u>GTTTTTTTATAGTTCATGTGCCGAACAACTACCGTT S'ss	
	rΟ		19
		TCAAGATGGGAGCCAGCCACTAACATCTCCTCTAGTTAACTTCACTGTCG branch site 3'ss	
	50	20 ATCAGATGCGATCCCTTATGGACAAGGTGTCCAACGTCCGTAACATGTCG (69
	70	. 70 GTTATTGCCCACGTTGATCACGGTAAGTCCACTTTAACTGACTCCCTGGT 119	119

FIG.

		GA!	-5: Pacti		AAGTT	-41 CTT	AAT	TTG	-31 PTC (CTCG:	-: LAGA	21 AA G/	AACG	-1: CATAC	1 3 AT	AATT(-1 CAAA
ATG	GTT	9 AAC	TTC	ACT	18 GTC	GAT	CAG	27 ATG	CGA	TCC	36 CTT	ATG	GAC	45 AAG	GTG	ACC	54 AAC
M	v	N	F	T	v	D	Q	М	R	s	L	M	D	ĸ	v	T	N
GTC	CGT	63 AAC	ATG	TCG	72 GTT	ATT	GCC	81 CAC	GTT	GAT	90 CAC	GGT	AAG	99 TCC	ACT	TTA	108 ACT
V	R	N	M	S	V	I	<u>A</u>	H	<u>v</u>	D	Н	G	K	s	T	L	T
GAC	TCC	117 CTG	GTG	CAA	126 CGT	GCC	GGT	135 ATT	ATT	TCT	144 GCT	GCC	AAG	153 GCT	GGT	GAG	162 GCC
D	s	L	V	Q	R	A	G	I	I	s	A	A	ĸ	A	G	E	A
CGT	TTC	ACT	GAT	ACT	180 AGA	AAG	GAC	189 GAG	CAA	GAG	198 AGA	GGT	ATC	207 ACC	ATC	AAG	216 TCT
R	F	(T)	D	T	R	K	<u>D</u>	Е	Q	E	R	G	I	т	I	ĸ	s
ACC	GCC	225 ATT	TCT	TTG	234 TAC	TCT	GAG	243 ATG	GGT	GAC	252 GAC	GAT	GTC	261 AAG	GAG	ATC	270 AAG
T	A	I	S	L	Y	s	E	M	G	D	D	D	V	K	E	I	ĸ
CAG	AAG	279 ACT	GAA	GGT	288 AAC	AGT	TTC	297 CTT	ATC	AAC	306 TTA	ATT	GAC	315 TCC	CCA	GGT	324 CAC
Q	K	T	E	G	N	s	F	L	I	N	L	I	D	s	P	G	H
GTT	GAC	333 TTC	TCT	TCT	342 GAG	GTC	ACT	351 GCT	GCT	CTG	360 CGT	GTT	ACT	369 GAC	GGT	GCT	378 TTG
V	D	F	S	S	E	V	T	A	A	L	R	v	T	D	G	A	L
GTC	GTC	387 GTT	GAC	TGT	396 GTT	GAA	GGT	405 GTC	TGT	GTT	414 CAA	ACT	GAG	423 ACC	GTT	TTG	432 CGT
V	V	V	D	С	V	E	G	v	C	v	Q	T	 E	T	v	r	R
CAA	GCT	441 TTG	GGT	GAA	450 AGA	ATC	AAG	459 CCA	GTT	GTT	468 GTC	ATT	AAC	477 AAG	GTC	GAC	486 CGT
Q	A	L	G	E	R	I	ĸ	P	v	v	v	ī	N	ĸ	v	D	R
GCT	CTT	495 TTG	GAG	TTG	504 CAA	GTT	ACC	513 AAG	GAG	GAC	522 CTG	TAC	CAG	531 TCT	TTC	GCT	540 AGA
A	L	L	E	L	Q	V	T	ĸ	E	D	L	Y	Q	s	F	Α	R
ACC	GTC	549 GAG	TCC	GTA	558 AAC	GTC	GTT	567 ATC	GCT	ACT	576 TAC	ACT	GAC	585 AAG	ACC	ATT	594 GGT
T	V	E	s	V	N	V	V	I	A	T	Y	T	D	K	T	I	G
GAC	AAC	603 CAA	GTC	TAC	612 CCA	GAA	CAG	621 GGT	ACC	GTC	630 GCT	TTC	GGT	639 TCA	GGT	CTG	
D	N	Q	V	Y	P	E	Q	G	T	v	A	F	G	s	G	r	н
GGA	TGG	657 GCT	TTC	ACC	666 GTT	AGA	CAG	675 TTC	GCC		684 AGA		TCC	693 AAG	AAG	TTC	702 GGT
G	W	A	F	T	V	R	Q	F	A		R		s	ĸ	ĸ	F	G

FIG. 3A

GTT	GAC	711 AGA	ATC	AAG	720 ATG	ATG	GAG	729 CGT	CTG	TGG	738 GGA	GAC	TCT	747 TAC	TTC	AAC	756 CCA
		R	ī			 М	 E	 R		w	 G		 s		 F		P
		765			774			783			792			801			810
			AAA 					GAC	AAG	GAC	GCC	GCT	GGA	AAG	CCT	TTG	GAG
K	T	K	K	W	T	N	K	D	K	D	A	A	G	K	P	L	E
CGT	GCC	819 TTC	AAC	ATG	828 TTC	GTT	TTG	837 GAC	CCT	ATC	846 TTC	CGT	CTG	855 TTT	GCT	GCC	864 ATC
R	A	F	N	м	F	v	L	D	 P	ī	 F	 R	L L	 F	 A	 A	 I
		873			882			891			900			909			918
ATG	AAC	TTC	AAG	AAG	GAT	GAA	ATT 	CCA	GTT	CTG	TTG	GAG	AAA 	TTG	GAG	ATC	AAC
М	N	F	K	K	D	E	I	P	v	L	L	E	K	L	E	I	N
CTG	AAG	927 CGT	GAG	GAG	936 AAG	GAG	TTG	945 GAG	GGT	AAG	954 GCT	CTT	TTG	963 AAG	GTT	GTC	972 ATG
L	ĸ	R	E	E	K	E	L	E	G	ĸ	A	L	L	к	v	v	м
202		981			990			999		:	1008		1	L017		1	1026
			TTG									ATG	ATT	GTT 	CTT	CAC	CTG
R		F	L		A	A	D	A	L	L	E	M	I	V	L	H	L
CCA		CCA	GTC		GCT	CAA		LO53 TAC	AGA	GCC	L062 GAG	ACT	TTG	LO71 TAC	GAA	GGT	LOSO CCA
 P			v		 A	Q	 A		 R	 A		 T	 L	 Y		 G	 P
		1089			1098			1107			1116		1	L125			1134
mom	0 3 M	CAC															
	GAT		CAA	TTC	TGC	ATT	GGT	ATC	AGA	GAG	TGT	GAC	CCT	AAG	GCT	GAG	CTG
5 5	D D	D D	CAA Q	TTC F	TGC C	ATT I	GGT G	ATC I	AGA R	GAG E	TGT C	GAC D	CCT P	AAG K	GCT A	GAG E	CTG L
S	D	D 1143	Q	F	C L152	ī	G	I 1161	R	E	 C L170	D	P	K 1179	Α	E	L 1188
S ATG	D	D 1143 TAC	Q	F TCC	C 1152 AAG	I	GTG	I 1161 CCA	R ACC	E	C 1170 GAC	D AAA	P	K 1179 AGA	A TTC	E	L 1188 GCC
S	D GTT V	D 1143 TAC Y	Q	TCC 	C L152 AAG K	I	G GTG V	I 1161 CCA P	R	E TCC S	C L170 GAC D	D	PGGT	K 1179 AGA R	Α	E TAC Y	L 1188 GCC A
S ATG M	D GTT V	D 1143 TAC Y	Q	TCC S	C L152 AAG K L206	I ATG M	GTG V	I 1161 CCA P	ACC T	E TCC S	C L170 GAC D	D AAA K	P GGT G	K 1179 AGA R	TTC F	E TAC Y	L 1188 GCC A
S ATG M	D GTT V	D 1143 TAC Y 1197 CGT	Q ATT	TCC S	C L152 AAG K L206	I ATG M	GTG V	I 1161 CCA P 1215 GTT	ACC T	E TCC S	C L170 GAC D	D AAA K	P GGT G	K 1179 AGA R	TTC F	E TAC Y	L 1188 GCC A
ATG M TTC	D GTT V GGT	D 1143 TAC Y 1197 CGT R	Q ATT I GTT V	TCC S	C 1152 AAG K 1206 TCC S	ATG M GGT G	GTG V ACT	I 1161 CCA P 1215 GTT V	ACC T AAG K	E TCC S	C 1170 GAC D 1224 GGT G	AAA K CAA	P GGT G	K 1179 AGA R 1233 GTC V	TTC F	TAC Y	L 1188 GCC A 1242 CAA Q
ATG M TTC F	GTT V GGT G	D 1143 TAC Y 1197 CGT R 1251 AAC	Q ATT I GTT V	TCC S	C 1152 AAG K 1206 TCC S 1260 CCA	ATG M GGT G GGT	GTG V ACT T	I 1161 CCA P 1215 GTT V 1269 AAG	ACC T AAG K GAG	E TCC S TCC S	C 1170 GAC D 1224 GGT G 1278 TTG	AAA K CAA Q TTC	P GGT G AAG K	1179 AGA R 1233 GTC V	A TTC F	E TAC Y ATC I	L 1188 GCC A 1242 CAA Q
ATG M TTC	GTT V GGT G	1143 TAC Y 1197 CGT R 1251 AAC	Q ATT I GTT V	TCC S	C 1152 AAG K 1206 TCC S 1260 CCA P	ATG M GGT G	GTG V ACT T	I 1161 CCA P 1215 GTT V 1269 AAG	ACC T AAG K	E TCC S GAC D	C GAC D L224 GGT G L278 TTG L	AAA K CAA	P GGT G AAG K ATC	K L179 AGA R L233 GTC V L287 AAG	TTC F	TAC Y ATC I GTT	L 1188 GCC A 1242 CAA Q
ATG M TTC F	GTT V GGT G CCT P	D 1143 TAC Y 1197 CGT R 1251 AAC N 1305	Q ATT I GTT V	TCC S TTC F	C 1152 AAG K 1206 TCC S 1260 CCA P 1314	ATG M GGT G GGT	GTG V ACT T AAG	I 1161 CCA P 1215 GTT V 1269 AAG K	ACC T AAG K GAG E	E TCC S GAC D	C GAC D L224 GGT G L278 TTG L L L L L L L L L L L L L L L L L L	AAA K CAA Q TTC F	P GGT G AAG K ATC	K 1179 AGA R 1233 GTC V 1287 AAG	A TTC F AGA R GCT A	E TAC Y ATC I	L 1188 GCC
ATG M TTC F GGT G AGA	GTT V GGT G CCT P	D 1143 TAC Y 1197 CGT R 1251 AAC N	Q ATT I GTT V TAC	F TCC S TTC F CTT V ATG	C 1152 AAG	ATG M GGT G GGT G GGA	G GTG V ACT T AAG K AGA	I 1161 CCA P 1215 GTT V 1269 AAG K 1323 ACC	ACC T AAG K GAG E GTC	E TCC S TCCC S GAC	C 1170 GAC D 1224 GGT G 1278 TTG L 1332 CCT	D AAAA K CAAA Q TTC F	GGT G AAG ATC I	K 1179 AGA R 1233 GTC V 1287 AAG K	A TTC F AGA R GCT A	E TAC Y ATC I GTT V CCA	L 1188 GCC
ATG TTC GGT G AGA R	D GTT V GGT G G CCT P	D 1143 TAC Y 1197 CGT R 1251 AAC N 1305 GTT V	Q ATT I GTT V TAC Y	F TCC S TTCC F TTCC ATG	C 1152 AAG	ATG M GGT G GGA GGA	GTG V ACT T AAG K AGA R	I 11161 CCA P 1215 GTT V 1269 AAG K 1323 ACC	ACC T AAG K GAG E GTC V	TCC S TCC S GAC GAG E	C 1170 GAC D 1224 GGT G L 1278 TTG L 1332 CCT P 1386	D AAA K CAA Q TTC F ATT	P GGT G AAG K ATC I GAC D	K 1179 AGA R 1233 GTC V 1287 AAG K 1341 GAT D	TTC F AGA R GCT A	E TAC Y ATC I CCA	L 1188 GCC A 1242 CAA Q 1296 CAA Q
S ATG	D GTT V GGT G CCT P ACT T	D 1143 TAC Y 1197 CGT R 1251 AAC V 1305 GTT V	Q ATT I GTT V TAC Y TTG L CTG	F TCC S TTCC F GTT V ATG	C 1152 AAG	ATG M GGT G GGA GTG G GTG	G GTG V ACT T AAG K AGA R GGT	I 11161 CCA P 1215 GTT V 1269 AAG ACC T T 1377 ATC	ACC T AAG K GAG E GTC V	E TCC S TCC S GAC D GAG CAG	C 1170 GAC D 1224 GGT G 1278 TTG L 1332 CCT P 1386 TTC	AAAA	P GGT G AAG K ATC I GAC CTG	K 1179 AGA R 1233 GTC V 1287 AAG K 1341 GAT D	A TTC F AGA R GCT V TCT	E TAC Y ATC I CCA P GGT	L 1188 GCC
ATG TTC GGT G AGA R	D GTT V GGT G CCT P ACT T	D 1143 TAC Y 1197 CGT R 1251 AAC V 1305 GTT V	Q ATT I GTT V TAC Y	F TCC S TTCC F GTT V ATG	C 1152 AAG	ATG M GGT G GGT G GGA GTG V	G GTG V ACT T AAG R AGA G G G	I 11161 CCA P 1215 GTT V 1269 AAG 	ACC T AAG K GAG E GTC V	E TCC S TCC S GAC D GAG E	C 1170 GAC D 1224 GGT G 1278 TTG L 1332 CCT P 1386 TTC	AAAA	P GGT G AAG K ATC I GAC CTG	K 1179 AGA R 1233 GTC V 1287 AAG K 1341 GAT D	A TTC F AGA R GCT V TCT	E TAC Y ATC I CCA P GGT	L 1188 GCC
S ATG	D GTT V GGT G CCT P ACT T AACC N	D 1143 TAC Y 1197 CGT R 1251 AAC N 1305 GTT V 1359 ATT I	Q ATT I GTT V TAC Y TTG L	F TCC S S TTC F GTT V ATG ATG GGT GGT GGT GGT GGT GGT GGT GGT	C 1152 AAG	ATG M GGT G GGA G GTG V	G GTG V ACT T AAG R AGA R GGT G G 5'EF	I 1161 CCA P 1215 GTT V 1269 AAG K 1323 ACC T 1377 T ATC T 1	AAG	E TCC S TCC S GAC CAG Q	C 1170 GAC D 1224 GGT G L 278 TTG L 1332 CCT F L 1386 TTC F	AAA K CAA Q TTC F ATT I TTG L	P GGT G AAG K ATC I GAC D CTG	K 1179 AGA R 1233 GTC V 1287 AAG K 1341 GAT D 1395 AAG K	A TTC F AGA R GCT A GTC V TCT	E TAC Y ATC I CCA P GGT G	L 1188 GCC A 1242 CAA Q 1296 CAA Q 1350 GCT A
S ATG	D GTT V GGT G G CCT P ACT T AAC	D 1143 TAC Y 1197 CGT N 1305 GTT U 1359 ATT I 1413	Q ATT I GTT V TAC Y TTG L CTG	F TCC S S TTC F GTT V ATG GGT G GGA	C 1152 AAG	ATG M GGT G GGT G GGA GCT GCT V	G GTG V ACT T AAG R AGA R GGT G CAC	I 1161 CCA P 1215 GTT V 1269 AAG ACC T 1377 ATC I 1431 AAC	ACC T AAG K GAG E GTC V GAC D	E TCC S TCC S GAC D GAG C AAG	C 1170 GAC D 1224 GGT TTG L 1332 CCT F 14440 GTG	AAA K CAA Q TTC F ATT I TTG L	P GGT G AAG K ATC I GAC CTG L	K 1179 AGA R 1233 GTC V 1287 AAG K 1341 GAT D 1395 AAG K	A TTC F AGA R GCT A GTC V TCT S	E TAC Y ATC I CCA P GGT G GTC	L 1188 GCC A 1242 CAA Q 1296 CAA Q 1350 GCT A

FIG. 3B

CCA		1467 CTC		C mm	1476			1485			1494		:	1503		;	1512
			CAA	GTT	GCC	GTT	GAG	GTC	AAG	AAC	GCT	AAT	GAT	CTG	ccc	AAG	TTG
P	V	V	Q	V	A	V	E	V	K	N	A	N	D	L	P	K	L
GTT		GGT	CTG		L530 CGT		TCC	L539 AAG	TCT	GAC	1548 CCA	TGT	GTT	1557 TTA	ACC	TAC	1566 ATC
v	E	G	L	ĸ	R	L	s	ĸ	 S	D	P	С	v	L L	T		 I
	1	1575			1584		1	1593			1602			1611			1620
TCC	GAG	TCT	GGT	GAG	CAC	ATT			GGT	ACT	GGT	GAG	CTG	CAC	TTG	GAA	ATC
S	E	s	G	E	н	I	v	A	G	T	G	E	L	Н	L L		I
		1629			L638			1647			1656			1665			1674
TGT	TTG	CAA	GAT	CTG	CAA	GAC	GAC	CAC	GCT	GGT	GTC		CTG	AAG	ATT	TCT	CCT
С	L	Q	D	L	Q	D	D	Н		G	v		L	K	I	s	P
	1	1683		:	1692		1	L701		;	1710		:	1719		:	1728
CCA	GTT 	GTT	ACC	TAC	CGT	GAG	ACT	GTC	ACT	AAC	GAA	TCT	TCC	ATG	ACT	GCC	CTG
P	V	V	T	Y	R	E	T	V	T	N	E	s	s	M	T	A	L
maa		1737			1746		:	1755		:	1764		:	1773			1782
TCC	AAG	TCT	CAG	AAC	AAG	CAT	AAC	AGA	ATT	TAC	CTG	AAG	GCT	CAA	CCA	ATT	GAC
s	K	S	Q	N	K	H	N	R	I	Y	L	K	A	Q	P	I	D
		791			1800		:	1809			1818		:	1827		:	1836
GAG	GAA	TTG	TCT	TTG	GCT	ATC	GAA	GAA	GGT	AAG	GTT	CAC	CCA	AGA	GAC	GAC	TTT
E	E	L	s	L	A	I	E	E	G	K	V	H	P	R	D	D	F
		L845			1854		1	1863			1872			1881			1890
AAA	GCC	AGA	GCC	AGA	ATC	ATG	GCT	GAT	GAA	TAC	GGT	TGG	GAC	GTC	ACT	GAT	GCC
K	A	R	A	R	I	M	A	D	E	Y	G	W	D	V	T	D	A
202		1899			1908		:	1917		:	1926		:	1935		:	1944
AGA	AAG	ATC	TGG	TGT	TTC	GGT	CCA	GAC	GGT	ACT	GGT	GCC	AAC	TTA	GTT	GTT	GAC
R	K	I	W	С	F	G	P	D	G	T	G	A	N	L	v	v	D
		1953			1962		:	1971			1980		:	1989			1998
CAG	TCT	AAG	GCT	GTC	CAA	TAC	TTG	CAC	GAG	ATC	AAG	GAC	TCT	GTT	GTT	GCC	GGT
Q	S	K	A	V	Q	Y	L	H	E	1	K	D	S	V	V	A	G
ጥጥር		2007 TTG	CCT	ACC.	2016	C33	com	2025	3 mm		2034			2043		:	2052
							GGT		ATT	TTG	GGA	GAA	AAC	ATG	AGA	TCC	GTC
F	Q	L	A	T	K	E	G	P	I	L	G	E	N	M	R	s	V
AGA		2061 AAC	ATC			ርጥጥ		2079			2088		200	2097 CAC		2	2106
			~						CAC 		GAT	GCT	ATC	CAC	AGA	GGT	GGA
R	V	N	I	L	D	<u>v</u>	T	L	Н	A	D	A	I	Н	R	G	G
GGA		GTC	ል ምጥ	CC ²	2124 ACC	አ ጥር	AAC	2133	Gmm	NCC.	2142	ccc		2151 TTC	or	m===	2160
															CTG	TTG	GCT
L_G_	Q	V	I	<u> P</u>	T	M	K	R] v	T	Y	A	A	F	L	L	A
GAG		2169		2	2178		:	2187		:	2196		2	2205		:	2214
-210	CCA	CCT	ልጥ ሮ	CAG	CAC	CCT	משת	Time	mm.a	000			a	me-			
E			ATC 			CCT P	ATC 	TTC F	TTG L	GTG	GAG	ATC	CAA	TGT	CCA	GAG	AAT

FIG. 3C

	2223 2232				:	2241			2250			2259	2268						
GCC	ATT	GGT	GGT	ATC	TAC	TCT	GTT	TTG	AAC	AAG	AAG	AGA	GGT	CAA	GTT	ATC	TCT		
A	I	G	G	I	Y	S	v	L	N	K	K	R	G	Q	v	I	s		
							_												
03.0	~~~	2211			2286			2295			2304		- 2	2313		:	2322		
GAG	GAA	CAA	AGA	CCA	GGT	ACC	CCA	TTG	TTC	ACT	GTC	AAA	GCT	TAC	TTG	CCA	GTT		
E	E	0	P	P		T			F	т	v	к							
_	_	~		-	G	1	P	ъ	F		٧	K	A	Y	L	P	V		
	:	2331		2	2340		:	2349		2	2358		2367				2376		
AAC	GAG	TCA	TTC	GGT	TTC	ACC	GGT	GAA	CTG	AGA	ÇAA	GCT	ACC	GCT	GGT	CAA	GCT		
N	Е	S	F	G	F	T	G	E	L	R	Q	Α	T	A	G	Q	A		
		2385			2394			2403		2	2412		- 2	2421			2430		
TTC	CCA	CAG	ATG	GTG	TTC	GAC	CAC	TGG	GCC	AAC	ATG	AAT	GGT	AAC	CCA	TTG	GAC		
E-		0	м	v	F	D	н												
E	F	Q	171	٧	F	ע	н	W	A	N	M	N	G	N	P	L	D		
	:	2439		2	2448		:	2457		3	2466			2475			2484		
CCA	GCC	TCC	AAG	GTC	GGT	GAG	ATT	GTT	CTT	GCT	GCC	AGA	AAG	AGA	CAG	GGT	ATG		
P	A	s	K	v	G	E	I	v	L	A	A	R	K	R	Q	G	M		
		2493																	
220			com.		2502			2511			2520			2529			2538		
AAG	GAG	AAC	GTT	CCT	GGT	TAT	GAA	GAG	TAC	TAC	GAC	AAG	TTG	TAA	GCT	TAA	TGT		
K	E	N	v	P	G	Y	E	E	Y	Y	D	ĸ	L						
	:	2547		2	2556		2	2565		2	2574		:	2583			2592		
TTC	ATT	AAC	TTA	TTT	GTG	TCG	TTC	GTA	TGT	CTA	TTT	ACG	TAC	TTA	ATT	CAG	TGT		
	A.	S'EF	-2◀																

2601 ATT GTT GTT 3'

FIG. 3D

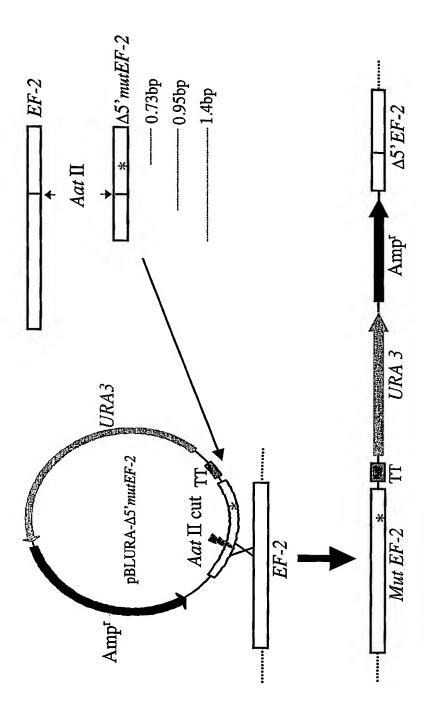


FIG. 4

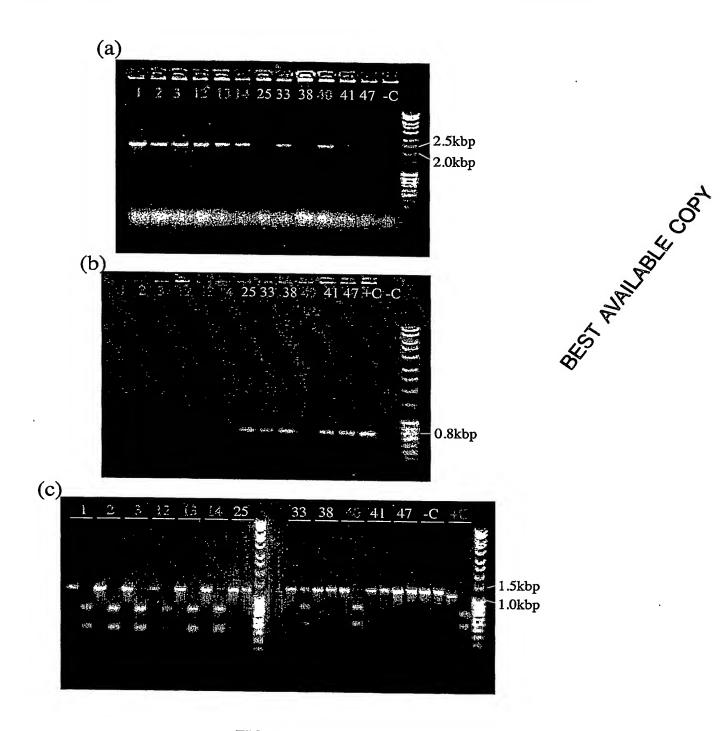
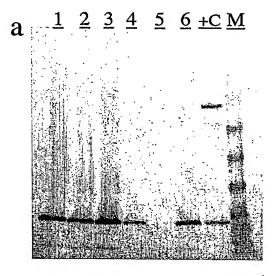


FIG. 5



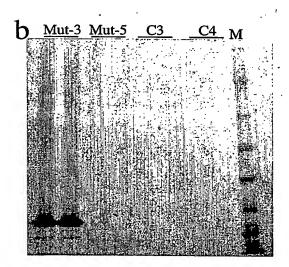


FIG. 6

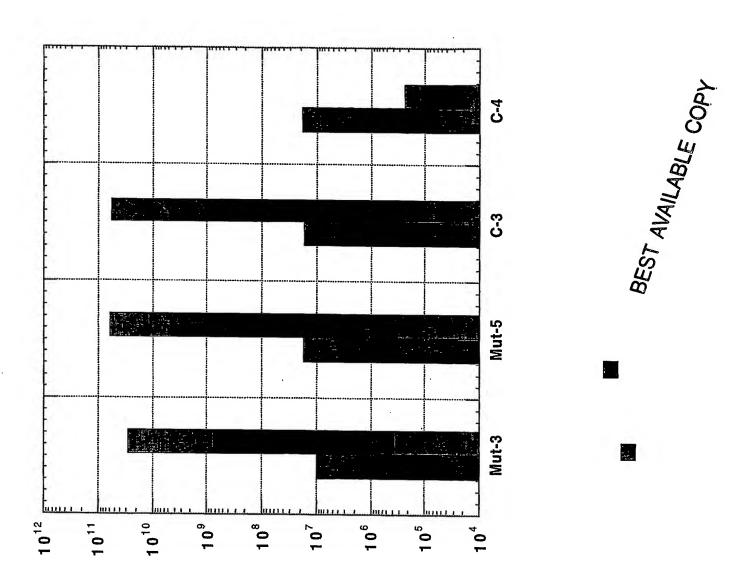


FIG. 7

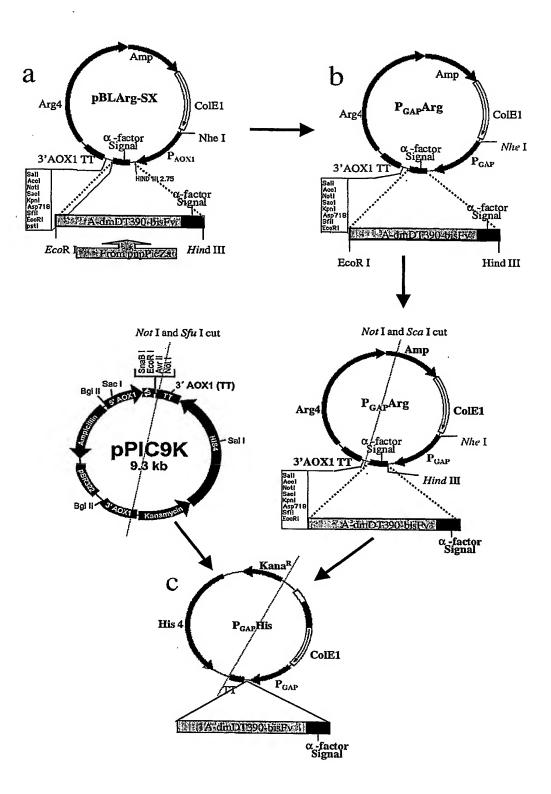


FIG. 8

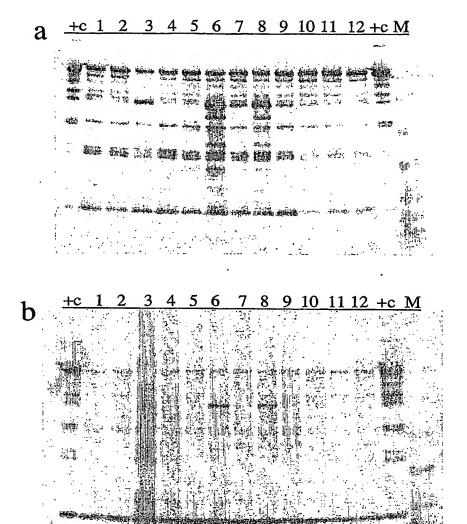


FIG. 9

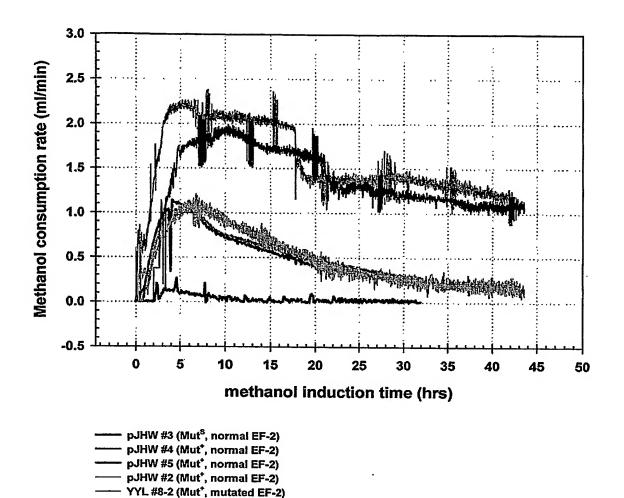


FIG. 10

X-33 with vector only (Mut*, normal EF-2)

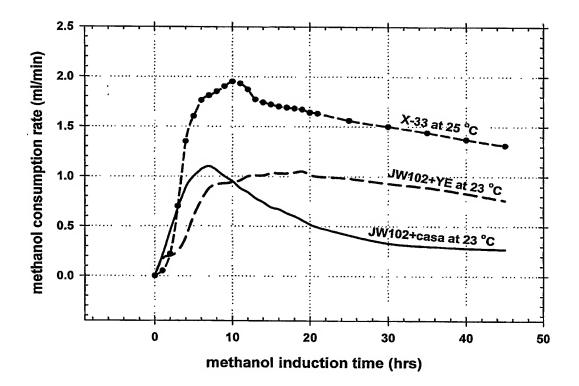


FIG. 11

Lowering agitation speed in fermentation reduces immunotoxin aggregates

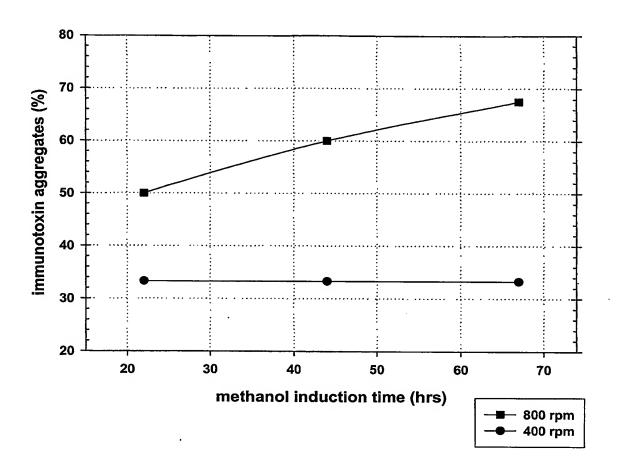


Fig. 12

Effect of Tween 20 on aggregation of purified immunotoxin after 20 hrs incubation at 30 C at 250 rpm

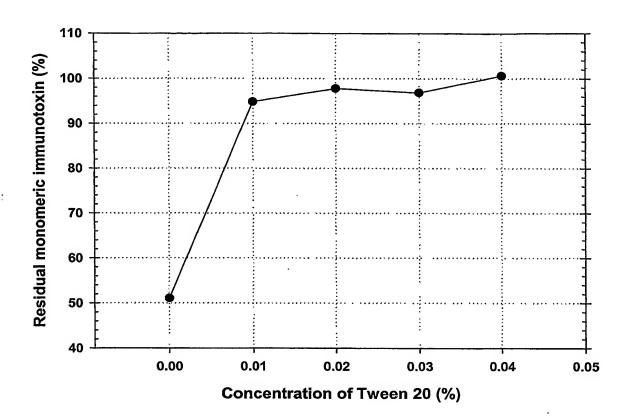


Fig. 13

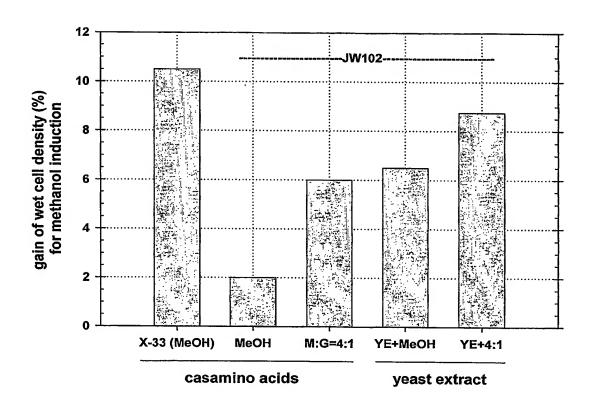


FIG. 14

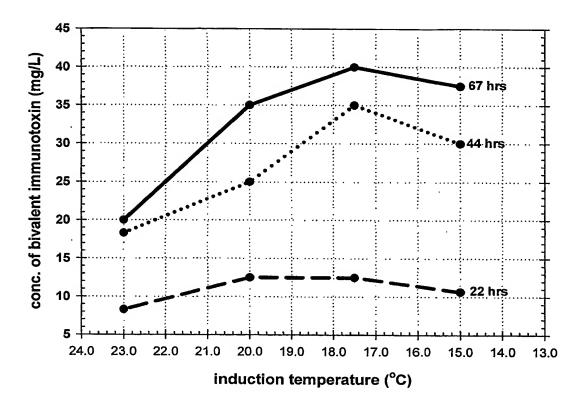


FIG. 15A

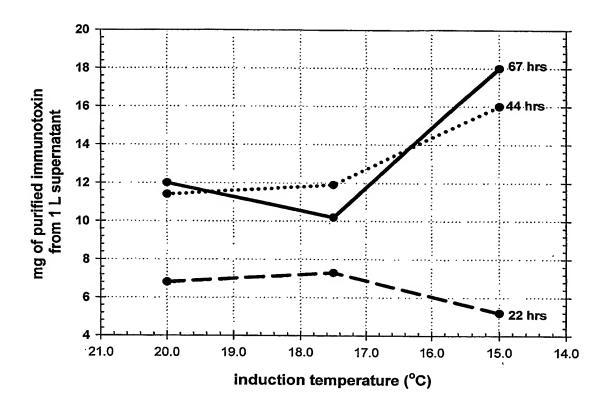


FIG. 15B

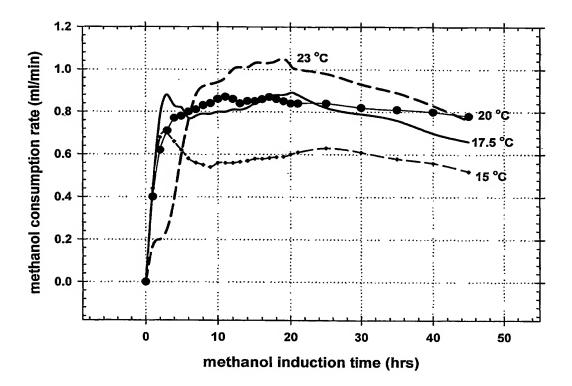


FIG. 15C

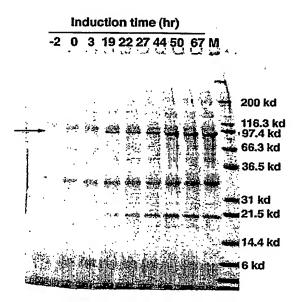


FIG. 16

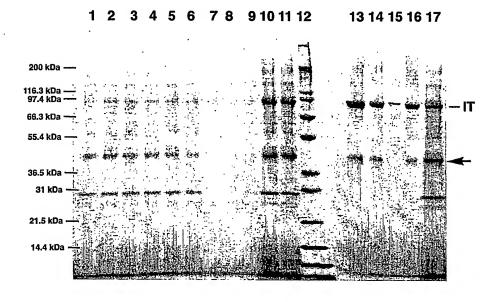


FIG. 17

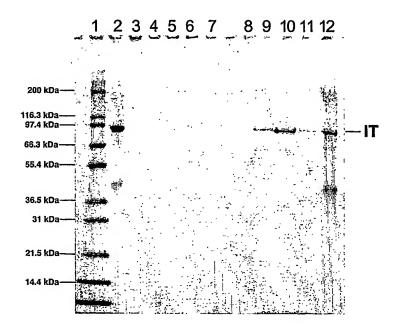


FIG. 18

PCT/US2004/024786

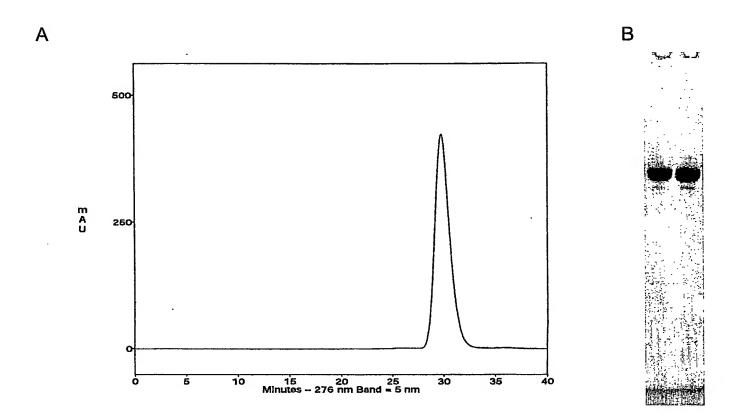


FIG. 19

Ala Gly Ala Asp Asp Val Val Asp Ser Ser Lys Ser Phe Val Met Glu

1 5 10 15

Asn Phe Ala Ser Tyr His Gly Thr Lys Pro Gly Tyr Val Asp Ser Ile

20 25 30

Gln Lys Gly Ile Gln Lys Pro Lys Ser Gly Thr Gln Gly Asn Tyr Asp

35 40 45 A5 Table Ob Share 25

Asp Asp Trp Lys Gly Phe Tyr Ser Thr Asp Asn Lys Tyr Asp Ala Ala 50 55 60

Gly Tyr Ser Val Asp Asn Glu Asn Pro Leu Ser Gly Lys Ala Gly Gly 65 70 75 80

Val Val Lys Val Thr Tyr Pro Gly Leu Thr Lys Val Leu Ala Leu Lys 85 90 95

Val Asp Asn Ala Glu Thr lie Lys Lys Glu Leu Gly Leu Ser Leu Thr 100 105 110

Glu Pro Leu Met Glu Gln Val Gly Thr Glu Glu Phe lle Lys Arg Phe 115 120 125

Gly Asp Gly Ala Ser Arg Val Val Leu Ser Leu Pro Phe Ala Glu Gly 130 135 140

Ser Ser Ser Val Glu Tyr Ile Asn Asn Trp Glu Gln Ala Lys Ala Leu 145 150 155 160

Ser Val Glu Leu Glu Ile Asn Phe Glu Thr Arg Gly Lys Arg Gly Gln 165 170 175

Asp Ala Met Tyr Glu Tyr Met Ala Gln Ala Cys Ala Gly Asn Arg Val 180 185 190

Arg Arg Ser Val Gly Ser Ser Leu Ser Cys lle Asn Leu Asp Trp Asp 195 200 205

Val le Arg Asp Lys Thr Lys Thr Lys Ile Glu Ser Leu Lys Glu His 210 215 220

Gly Pro lle Lys Asn Lys Met Ser Glu Ser Pro Ala Lys Thr Val Ser 225 230 235 240

Glu Glu Lys Ala Lys Gln Tyr Leu Glu Glu Phe His Gln Thr Ala Leu 245 250 255

Glu His Pro Glu Leu Ser Glu Leu Lys Thr Val Thr Gly Thr Asn Pro 260 265 270

Val Phe Ala Gly Ala Asn Tyr Ala Ala Trp Ala Val Asn Val Ala Gln 275 280 285

Val Ile Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Thr Ala Ala 290 295 300

Leu Ser Ile Leu Pro Gly Ile Gly Ser Val Met Gly Ile Ala Asp Gly 305 310 315 320

Ala Val His His Asn Thr Glu Glu lle Val Ala Gln Ser lle Ala Leu 325 330 335

Ser Ser Leu Met Val Ala Gln Ala Ile Pro Leu Val Gly Glu Leu Val 340 345 350

Asp Ile Gly Phe Ala Ala Tyr Asn Phe Val Glu Ser Ile Ile Asn Leu 355 360 365

Phe Gln Val Val His Asn Ser Tyr Asn Arg Pro Ala Tyr Ser Pro Gly 370 375 380

His Lys Thr Gin Pro Phe Leu Pro Trp Asp Ile Gin Met Thr Gin Thr 385 390 395 400

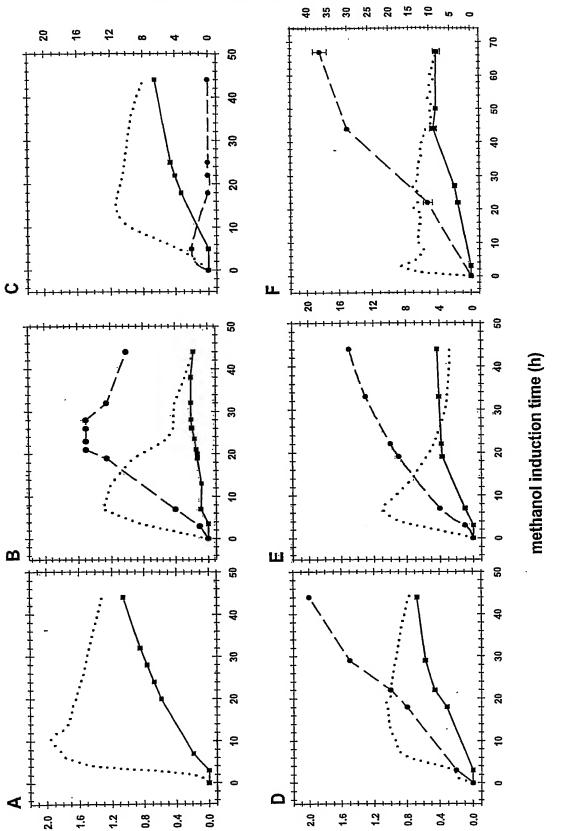
Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr Ile Ser Cys 405 410 415

Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr Gln Gln Lys 420 425 430

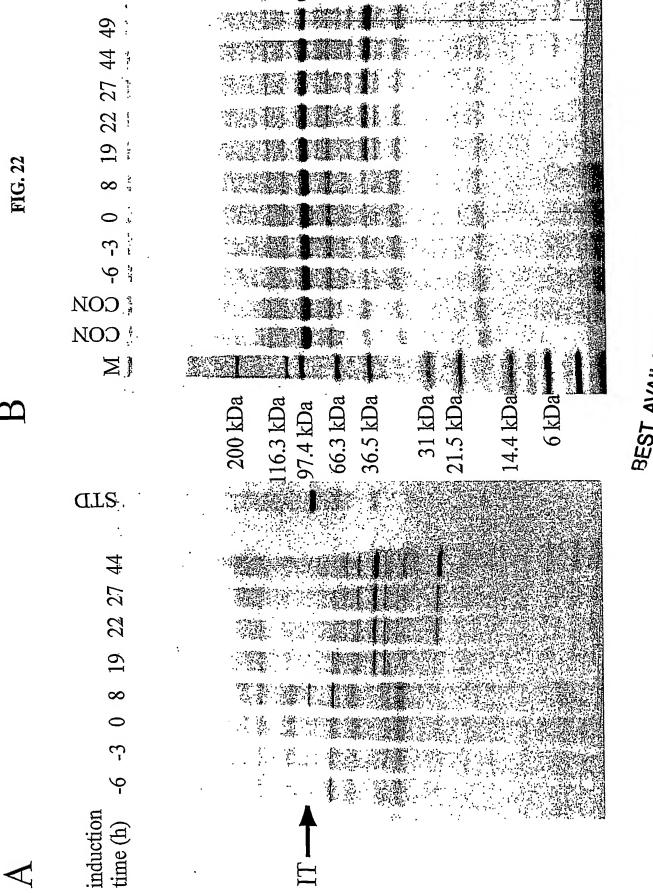
- Pro Asp Gly Thr Val Lys Leu Leu Ile Tyr Tyr Thr Ser Arg Leu His 435 440 445
- Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr 450 455 460
- Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala Thr Tyr Phe 465 470 475 480
- Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly Gly Thr Lys 485 490 495
- Leu Glu Ile Lys Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly 500 505 510
- Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys 515 520 525
- Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe 530 535 540
- Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly Lys Asn Leu 545 550 555 560
- Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser Thr Tyr Asn 565 570 575
- Gin Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys Ser Ser Ser 580 585 590
- Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp Ser Ala Val 595 600 605
- Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp Trp Tyr Phe 610 615 620
- Asp Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ser Gly Gly 625 630 635 640
- Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser Asp Ile Gln Met 645 650 655
- Thr Gln Thr Ser Ser Leu Ser Ala Ser Leu Gly Asp Arg Val Thr 660 665 670
- lle Ser Cys Arg Ala Ser Gln Asp Ile Arg Asn Tyr Leu Asn Trp Tyr 675 680 685
- Gln Gln Lys Pro Asp Gly Thr Val Lys Leu Leu lle Tyr Tyr Thr Ser 690 695 700
- Arg Leu His Ser Gly Val Pro Ser Lys Phe Ser Gly Ser Gly Ser Gly 705 710 715 720
- Thr Asp Tyr Ser Leu Thr Ile Ser Asn Leu Glu Gln Glu Asp Ile Ala 725 730 735
- Thr Tyr Phe Cys Gln Gln Gly Asn Thr Leu Pro Trp Thr Phe Ala Gly 740 745 750
- Gly Thr Lys Leu Glu lle Lys Gly Gly Gly Gly Gly Gly Gly 755 760 765
- Ser Gly Gly Gly Ser Glu Val Gln Leu Gln Gln Ser Gly Pro Glu 770 775 780
- Leu Val Lys Pro Gly Ala Ser Met Lys Ile Ser Cys Lys Ala Ser Gly 785 790 795 800
- Tyr Ser Phe Thr Gly Tyr Thr Met Asn Trp Val Lys Gln Ser His Gly 805 810 815
- Lys Asn Leu Glu Trp Met Gly Leu Ile Asn Pro Tyr Lys Gly Val Ser 820 825 830

Thr Tyr Asn Gln Lys Phe Lys Asp Lys Ala Thr Leu Thr Val Asp Lys 835 840 845
Ser Ser Ser Thr Ala Tyr Met Glu Leu Leu Ser Leu Thr Ser Glu Asp 850 855 860
Ser Ala Val Tyr Tyr Cys Ala Arg Ser Gly Tyr Tyr Gly Asp Ser Asp 865 870 875 880
Trp Tyr Phe Asp Val Trp Gly Gln Gly Thr Thr Leu Thr Val Phe Ser 885 890 896

increase in wet cell density (%) or secretion level of immunotoxin (mg/L) during methanol induction



•



BEST AVAILABLE COPY

methanol induction temp (⁰C) 44 50 67 M 116.3 kd 97.4 kd 66.3 kd 36.5 kd 31 kd 21.5 kd



